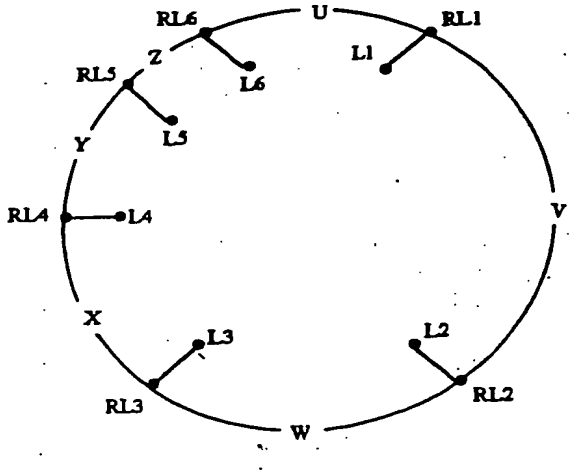
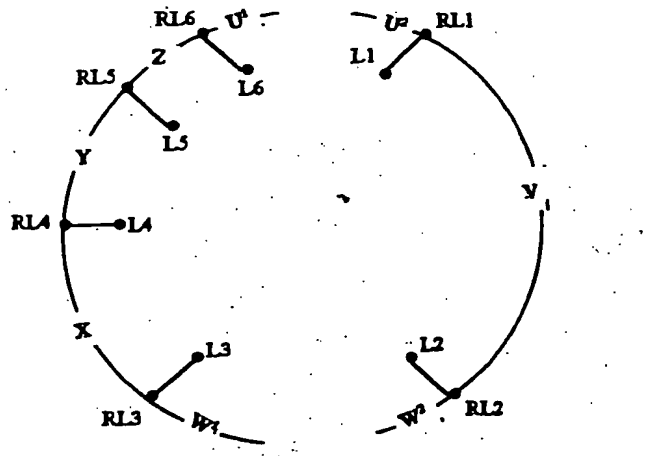
AMENDMENTS TO THE CLAIMS

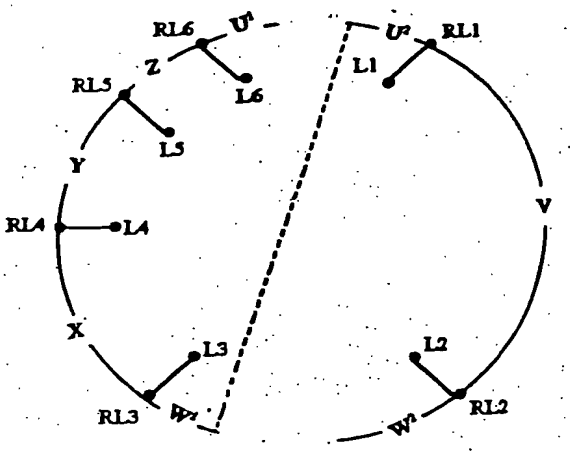
1. (Previously Presented) A chemical structure with an affinity for a phospholipid, comprising a chemical platform U, V, W, X, Y including six residues RL1, RL2, RL3, RL4, RL5, RL6 supporting a set of chemical functions which may bind to said phospholipid, called, L1, L2, L3, L4, L5, L6 respectively, wherein these chemical functions L define at least partly the affinity of said structure for said phospholipid, said structure having one of the following constructions (I), (II) and (III):



(I)



(II)



(III)

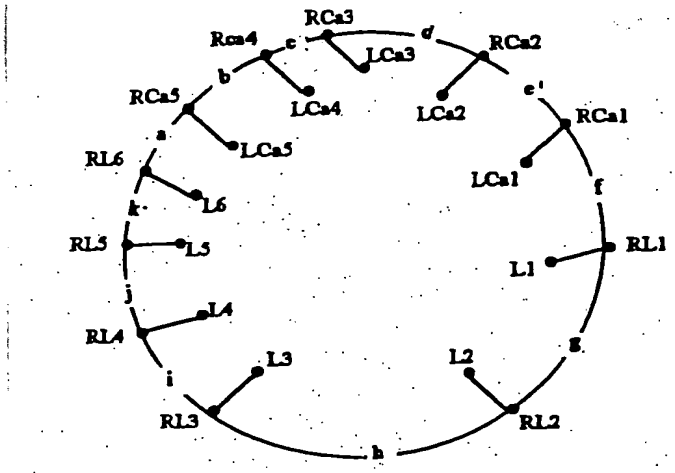
wherein U, U^1, U^2, V, W, W^1, W^2, X, Y, Z are independently a natural or non-natural amino-acid, a peptide consisting of natural or non-natural amino-acids, a carbon chain, or carbon cyclic group(s),

wherein RL1 to RL6 are selected from molecules having the binding chemical functions L1 to L6, respectively, wherein said chemical functions comprise either at least a positive charge, donor of a hydrogen bond, or at least a negative charge, acceptor of a hydrogen bond, and

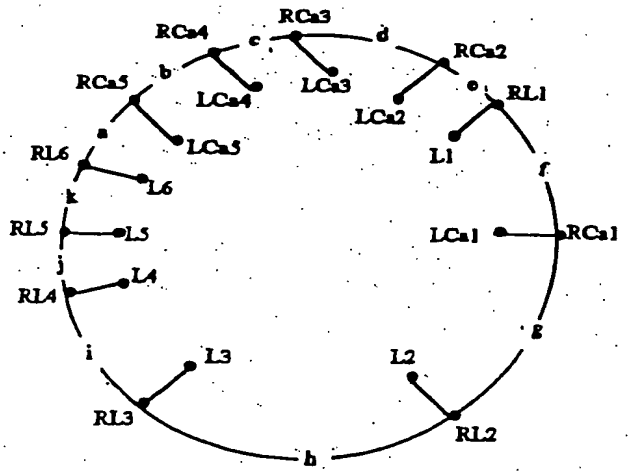
wherein U, U^1, U^2, V, W, W^1, W^2, X, Y, Z are such that RL6 and RL1 are distant from 0.65 to 0.95 nm, L6 and L1 are distant from 0.65 to 0.9 nm, RL1 and RL2 are distant from 0.45 to 0.65 nm, L1 and L2 are distant from 0.4 to 0.55 nm, RL2 and RL3 are distant from 0.5 to 1.05 nm, L2 and L3 are distant from 0.4 to 0.6 nm, RL3 and RL4 are distant from 0.5 to 0.8 nm, L3 and L4 are distant from 0.35 to 0.5 nm, RL4 and RL5 are distant from 0.45 to 0.75 nm, and L4 and L5 are distant from 0.4 to 0.55 nm, RL5 and RL6 are distant from 0.4 to 1.2 nm, L5 and L6 are distant from 0.4 to 0.6 nm.

2. (Previously Presented) The chemical structure with an affinity for a phospholipid,

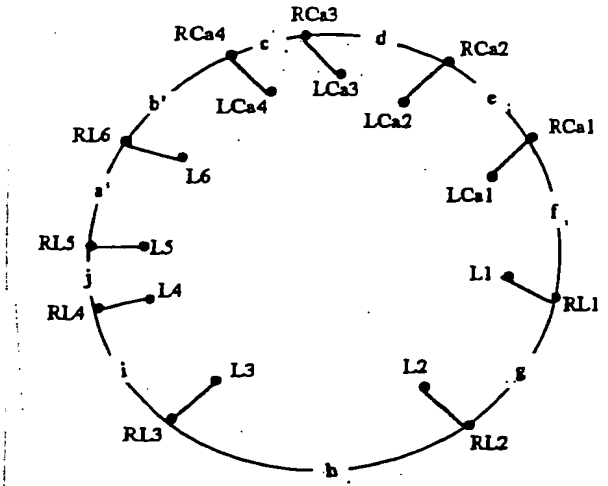
comprising a chemical platform a, a', b, b', c, d, e, f, g, h, i, j, k, l including 11 residues, LR1, LR2, LR3, LR4, LR5, RL6, RCa1, RCa2, RCa3, RCa4 and RCa5 supporting a set of chemical functions which may bind to said phospholipid called L1, L2, L3, L4, L5, L6, respectively, and a set of chemical functions binding to a calcium atom called LCa1, LCa2, LCa3, LCa4, LCa5, respectively, wherein these chemical functions RL1 to RCa5 define at least partly the affinity of said structure for said phospholipid, said structure having one of the following constructions (IV), (V) and (VI):



(IV)



(V)



(VI)

wherein a, a', b, b', c, d, e, f, g, h, i, j, k, l, are independently a natural or non-natural amino acid, a peptide consisting of natural or non-natural amino acids, a carbon chain, or carbon cyclic group(s),

wherein RL1 to RL6 and RCa1 to RCa5 are selected from molecules having chemical binding functions L1 to L6 and LCa1 to LCa5, respectively, wherein said chemical functions L1 to L6 comprise either at least a positively charged donor of a hydrogen bond, or at least a negatively charged acceptor of a hydrogen bond, said chemical functions LCa1 to LCa5 comprising an oxygen atom, and

wherein a in the structures of construction (IV) and (V) is such that RL6 and RCa5 are distant from 0 to 0.35 nm and such that L6 and LCa5 are distant from 0 to 0.3 nm, b in the structures of construction (IV) and (V) is such that RCa5 and RCa4 are distant from 0 to 0.35 nm and such that LCa5 and LCa4 are distant from 0.2 to 0.3 nm, b' in the structure of

construction (VI) is such that RL6 and RCa4 are distant from 0 to 0.35 nm and such that L6 and LCa4 are distant from 0 to 0.35 nm, c and d are such that RCa4 and RCa3 are distant from 0.5 to 0.9 nm, LCa4 and LCa3 are distant from 0.2 to 0.4 nm, RCa3 and RCa2 are distant from 0.35 to 0.6 nm, and LCa3 and LCa2 are distant from 0.22 to 0.3 nm, e, f, g, in the structures of construction (IV), (V), (VI) are such that RL1 and RL2 are distant from 0.45 to 0.65 nm, RCa1 to RCa2 are distant from 0.4 to 0.55 nm, L1 and L2 are distant from 0.4 to 0.55 nm and LCa1 and LCa2 are distant from 0.3 to 0.4 nm, h, i, j and k are such that RL2 and RL3 are distant from 0.5 to 1.05 nm, L2 and L3 are distant from 0.4 to 0.6 nm, RL3 and RL4 are distant from 0.5 to 0.8 nm, L3 and L4 are distant from 0.35 to 0.5 nm, RL4 and RL5 are distant from 0.45 to 0.75 nm, L4 and L5 are distant from 0.4 to 0.55 nm, RL5 and RL6 are distant from 0.4 to 1.2 nm, and L5 and L6 are distant from 0.4 to 0.6 nm, a' in the structure of construction (VI) is such that RL5 and RL6 are distant from 0.4 to 1.2 nm and such that L5 and L6 are distant from 0.4 to 0.6 nm, and b' in the structure of construction (VI) is such that RL6 and RCa4 are distant from 0 to 0.35 nm and such that L6 and LCa4 are distant from 0 to 0.35 nm, wherein the structure may either be closed or open at a and/or at h.

3. (Original) The chemical structure according to claim 1, wherein L1, L2, L3 and L6 each have at least a positively charged donor of a hydrogen bond, and L4 and L5 each have at least a negatively charged acceptor of a hydrogen bond.

4. (Original) The chemical structure according to claim 1, wherein U, V, W, X, Y and Z are peptides consisting of natural and non-natural amino acids, and RL1 to RL6 are amino acids selected from a set comprising Lys, Arg, Orn, Ser, Thr, Asp and Glu, or analogs of the latter, L1 to L6 are the charge-bearing functions of the side chains of said amino acids.

5. (Currently Amended) The chemical structure according to claim 1, wherein RL1, RL2, and RL3 ~~and RL6~~ are independently selected from Arg, Lys, Orn,

wherein RL4 is independently selected from Asp or Glu, and

wherein RL5 is independently selected from Ser, Thr, Asp or Glu, wherein the side chains of these amino acids have chemical functions for binding to the phospholipids L1 to L6, respectively.

6. (Original) The chemical structure according to claim 3, wherein the chemical binding functions L1 to L6 are directly accessible to the negatively charged phospholipid.

7. (Original) The chemical structure according to claim 1, further comprising a calcium site where the calcium ion complexed by this site is one of the ligands of the phospholipid.

8. (Original) The chemical structure according to claim 2, wherein a or a', b or b', c, d, e, f, g, h, i, j, k are peptides consisting of natural or non-natural amino acids, and RL1 to RL6 are amino acids selected from a set comprising Lys, Arg, Orn, Ser, Thr, Asp and Glu, or analogs of the latter, L1 to L6 and LCa1 to LCa5 are the charge-bearing functions of the side chains of said amino acids, and RCa1 to RCa5 are natural or non-natural amino acids.

9. (Original) The chemical structure according to claim 8, wherein the chemical binding functions L1 to L6 and the positive charges of the calcium atom when it is bound to the binding functions LCa1 to LCa5, are directly accessible to the phospholipid.

10. (Previously Presented) The chemical structure according to Claim 1, wherein the platform is a portion of a domain of the annexin or of a modified domain of the annexin, comprising at least said residual ligands, RL1 to RL6, having said functions L1 to L6 for binding to the phospholipid respectively.

11. (Previously Presented) The chemical structure according to claim 10, wherein the annexin domain is selected from the domain 1 of annexin V corresponding to amino acid residues 16-91 of SEQ ID NO: 2, domain 2 of annexin I corresponding to amino acid residues

114-186 of SEQ ID NO: 1, domain 2 of annexin III corresponding to amino acid residues 90-162 of SEQ ID NO: 3, domain 1 of annexin IV corresponding to amino acid residues 15-85 of SEQ ID NO: 4, and domain 2 of annexin IV corresponding to amino acid residues 1-75 of SEQ ID NO: 5.

12. (Previously Presented) The chemical structure according to claim 11, wherein the residual ligands RL1 to RL6 respectively are either the residues Arg25, Lys29, Arg63, Asp68, Ser71 and Glu72 of domain 1 of annexin V corresponding to amino acid residues 16-91 of SEQ ID NO: 2 or residues Arg124, Lys128, Arg162, Asp167, Ser170 and Asp171 of domain 2 of annexin I corresponding to amino acid residues 114-186 of SEQ ID NO: 1, or residues Lys100, Lys104, Lys138, Asp143, Ser146 and Glu147 of domain 2 of annexin III corresponding to amino acid residues 90-162 of SEQ ID NO: 3, or residues Arg97, Lys101, Arg135, Asp140, Ser143 and Asp144 of domain 2 of annexin IV corresponding to amino acid residues 1-75 of SEQ ID NO: 5, or residues Arg24, Lys28, Arg62, Asp67, Ser70 and Glu71 of domain 1 of annexin IV corresponding to amino acid residues 15-85 of SEQ ID NO: 4.

13. (Currently Amended) A chemical structure with an affinity for a phospholipid, comprising a molecule with the following formula (VII):

$$RL1\text{-}N^{1}\text{-}RL2\text{-}M\text{-}RL3\text{-}N^{2}\text{-}RL4\text{-}N^{3}\text{-}RL5\text{-}RL6$$

(VII)

wherein N^1 to N^3 each independently represent 1 to 4, independently selected, natural or non-natural, amino acids and wherein M is a peptide consisting of 1 to 100 natural or non-natural amino acids;

wherein RL1, RL2, and RL3 ~~and RL6~~ are independently selected from Lys, Arg or

Orn; RL4 and RL6 are ~~is~~ independently selected from Asp or Glu; and RL5 is independently selected from Ser, Thr, Asp, or Glu, wherein said structure is linear or cyclic.

14. (Previously Presented) The chemical structure according to claim 13, wherein N^1 represents three amino acids, N^2 represents four amino acids, and N^3 represents two amino acids.

15. (Previously Presented) The chemical structure according to Claim 13, wherein M is a peptide consisting of 33 natural or non-natural amino acids.

16. (Currently Amended) The chemical structure according to claim 13, wherein the structure of formula (VII) is a peptide sequence selected from the peptide sequence from Arg124 to ~~Ser171~~ Asp171 of SEQ ID NO: 1, the peptide sequence from Arg25 to Glu72 of SEQ ID NO: 2, the peptide sequence from Lys100 to Glu147 of SEQ ID NO: 3, the sequence from Arg24 to Glu71 of SEQ ID NO: 4, the sequence from Arg97 to Asp144 of SEQ ID NO: 5 or a modified sequence of these sequences provided that RL1, RL2, and RL3 ~~and RL6~~ are independently selected from Lys, Arg or Orn; RL4 and RL6 are ~~is~~ independently selected from Asp or Glu; and RL5 is independently selected from Ser, Thr, Asp, or Glu.

17. (Previously Presented) A chemical structure with an affinity for a phospholipid, comprising at least a portion of a peptide sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5 or a modified sequence of the latter.

18. (Currently Amended) A chemical structure with an affinity for a negatively charged phospholipid, comprising a cyclic peptide sequence of the following formula (VIII):

Gly-RL1-Phe-RL2-P^1-Gly-Tyr-P^2-RL3-P^3-RL4-Q^1-RL5-Trp-RL6

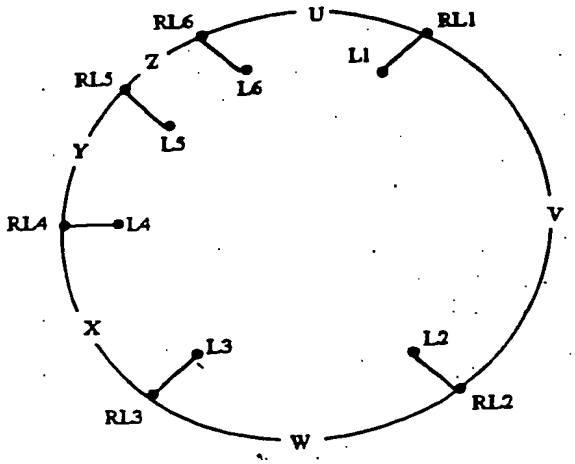
wherein RL1 ~~and RL6~~ are independently selected from Lys, Orn and Arg; RL2 and RL3 are Arg; RL4, RL5, and RL6 ~~and RL5~~ are independently selected from Asp and Glu;

wherein P^1, P^2 and P^3 are independently selected from Ser and Thr; wherein Q^1 is selected from Gly and Met.

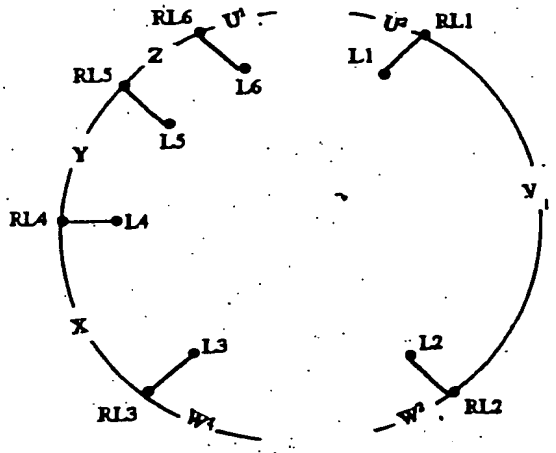
19. (Previously Presented) The chemical structure according to Claim 13, further comprising a calcium site where the calcium ion is complexed by this site forms one of the ligands of the negatively charged phospholipid.

20. (Previously Presented) The chemical structure according to Claim 1, said structures having an affinity for a phospholipid selected from a phosphatidylserine, a phosphatidylethanolamine, a phosphatidylinositol, a phosphatidic acid, and a cardiolipin.

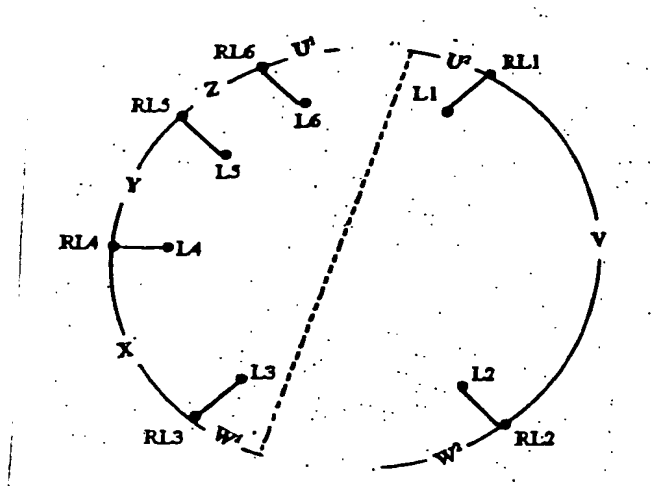
21. (Currently Amended) A chemical assembly having an affinity for a phospholipid, comprising at least two identical or different chemical structures selected from the group consisting of A, B, C, D and E where A is a chemical structure with an affinity for a phospholipid, consisting of at least a chemical platform U, V, W, X, Y, Z including six residues RL1, RL2, RL3, RL4, RL5, RL6 supporting a set of chemical functions which may bind to said phospholipid, called, L1, L2, L3, L4, L5, L6 respectively, wherein these chemical functions L define the affinity of said structure for said phospholipid, said structure having one of the following constructions (I), (II) and (III):


U
RL1
L1
V
L2
RL2
W
L3
RL3
X
RL4
L4
Y
RL5
L5
Z
RL6
L6

(I)


RL1
L1
L2
RL2
L3
RL3
RL4
L4
RL5
L5
RL6
L6

(II)



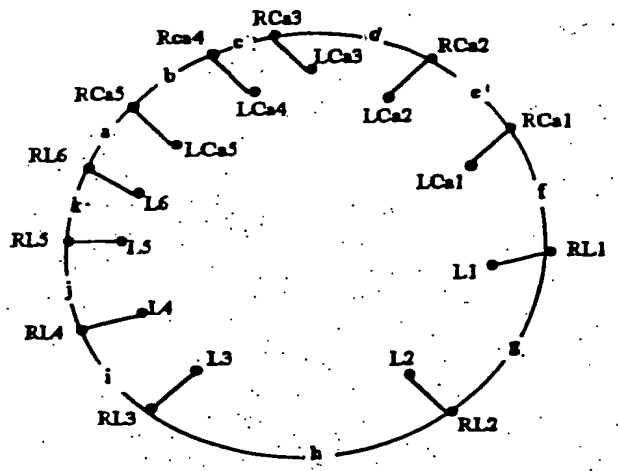
(III)

wherein U, U^1, U^2, V, W, W^1, W^2, X, Y, Z are independently a natural or non-natural amino-acid, a peptide consisting of natural or non-natural amino-acids, a carbon chain, or carbon cyclic group(s),

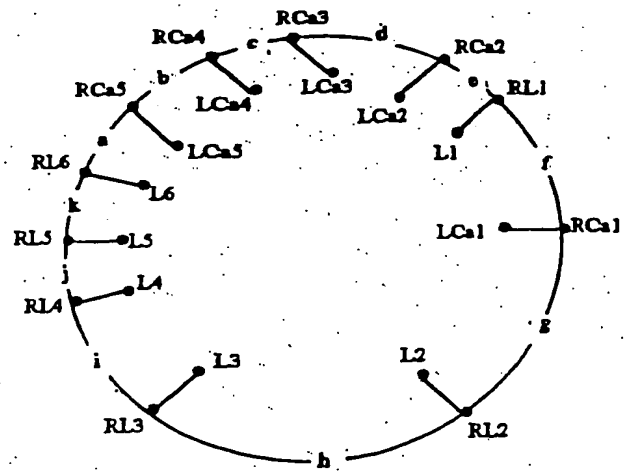
wherein RL1 to RL6 are selected from molecules having the binding chemical functions L1 to L6, respectively, wherein said chemical functions comprise either at least a positive charge, donor of a hydrogen bond, or at least a negative charge, acceptor of a hydrogen bond, and

wherein U, U^1, U^2, V, W, W^1, W^2, X, Y, Z are such that RL6 and RL1 are distant from 0.65 to 0.95 nm, L6 and L1 are distant from 0.65 to 0.9 nm, RL1 and RL2 are distant from 0.45 to 0.65 nm, L1 and L2 are distant from 0.4 to 0.55 nm, RL2 and RL3 are distant from 0.5 to 1.05 nm, L2 and L3 are distant from 0.4 to 0.6 nm, RL3 and RL4 are distant from 0.5 to 0.8 nm, L3 and L4 are distant from 0.35 to 0.5 nm, RL4 and RL5 are distant from 0.45 to 0.75 nm, and L4 and L5 are distant from 0.4 to 0.55 nm, RL5 and RL6 are distant from 0.4

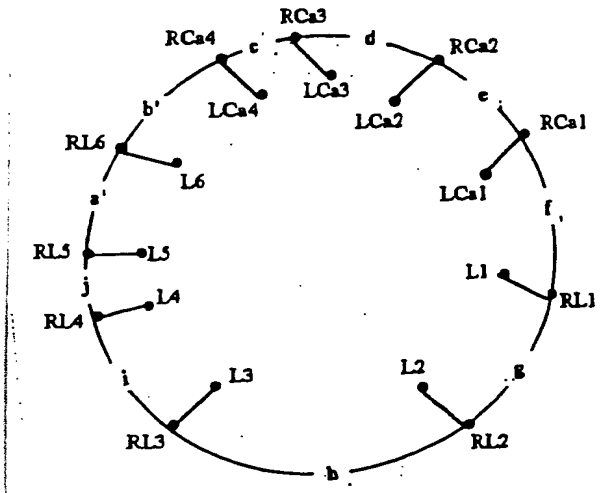
to 1.2 nm, L5 and L6 are distant from 0.4 to 0.6 nm, where B is a chemical structure with an affinity for a phospholipid, consisting of at least a chemical platform a, a', b, b', c, d, e, f, g, h, i, j, k, l including 11 residues, LR1, LR2, LR3, LR4, LR5, RL6, RCa1, RCa2, RCa3, RCa4 and RCa5 supporting a set of chemical functions which may bind to said phospholipid called L1, L2, L3, L4, L5, L6, respectively, and a set of chemical functions binding to a calcium atom called LCa1, LCa2, LCa3, LCa4, LCa5, respectively, wherein these chemical functions RL1 to RCa5 define the affinity of said structure for said phospholipid, said structure having one of the following constructions (IV), (V) and (VI):



(IV)



(V)



(VI)

wherein a, a', b, b', c, d, e, f, g, h, i, j, k, l, are independently a natural or non-natural amino acid, a peptide consisting of natural or non-natural amino acids, a carbon chain, or carbon cyclic group(s),

wherein RL1 to RL6 and RCa1 to RCa5 are selected from molecules having chemical binding functions L1 to L6 and LCa1 to LCa5, respectively, wherein said chemical functions L1 to L6 comprise either at least a positively charged donor of a hydrogen bond, or at least a negatively charged acceptor of a hydrogen bond, said chemical functions LCa1 to LCa5 comprising an oxygen atom, and

wherein a in the structures of construction (IV) and (V) is such that RL6 and RCa5 are

distant from 0 to 0.35 nm and such that L6 and LCa5 are distant from 0 to 0.3 nm, b in the structures of construction (IV) and (V) is such that RCa5 and RCa4 are distant from 0 to 0.35 nm and such that LCa5 and LCa4 are distant from 0.2 to 0.3 nm, b' in the structure of construction (VI) is such that RL6 and RCa4 are distant from 0 to 0.35 nm and such that L6 and LCa4 are distant from 0 to 0.35 nm, c and d are such that RCa4 and RCa3 are distant from 0.5 to 0.9 nm, LCa4 and LCa3 are distant from 0.2 to 0.4 nm, RCa3 and RCa2 are distant from 0.35 to 0.6 nm, and LCa3 and LCa2 are distant from 0.22 to 0.3 nm, e, f, g, in the structures of construction (IV), (V), (VI) are such that RL1 and RL2 are distant from 0.45 to 0.65 nm, RCa1 to RCa2 are distant from 0.4 to 0.55 nm, L1 and L2 are distant from 0.4 to 0.55 nm and LCa1 and LCa2 are distant from 0.3 to 0.4 nm, h, i, j and k are such that RL2 and RL3 are distant from 0.5 to 1.05 nm, L2 and L3 are distant from 0.4 to 0.6 nm, RL3 and RL4 are distant from 0.5 to 0.8 nm, L3 and L4 are distant from 0.35 to 0.5 nm, RL4 and RL5 are distant from 0.45 to 0.75 nm, L4 and L5 are distant from 0.4 to 0.55 nm, RL5 and RL6 are distant from 0.4 to 1.2 nm, and L5 and L6 are distant from 0.4 to 0.6 nm, a' in the structure of construction (VI) is such that RL5 and RL6 are distant from 0.4 to 1.2 nm and such that L5 and L6 are distant from 0.4 to 0.6 nm, and b' in the structure of construction (VI) is such that RL6 and RCa4 are distant from 0 to 0.35 nm and such that L6 and LCa4 are distant from 0 to 0.35 nm, wherein the structure may either be closed or open at a and/or at h, where C is a chemical structure with an affinity for a phospholipid, comprising a molecule with the following formula (VII):

$$RL1\text{-}N^{1}\text{-}RL2\text{-}M\text{-}RL3\text{-}N^{2}\text{-}RL4\text{-}N^{3}\text{-}RL5\text{-}RL6 \qquad (VII)$$

wherein N^{1} to N^{3} each independently represent 1 to 4, independently selected, natural or non-natural, amino acids and wherein M is a peptide consisting of 1 to 100 natural or non-

natural amino acids

wherein RL1, RL2, and RL3 ~~and RL6~~ are independently selected from Lys, Arg or Orn; RL4 and RL6 are ~~is~~ independently selected from Asp or Glu; and RL5 is independently selected from Ser, Thr, Asp, or Glu, wherein said structure is linear or cyclic, where D is a chemical structure with an affinity for a phospholipid, comprising at least a portion of a peptide sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5 or a modified sequence of the latter, where E is a chemical structure with an affinity for a negatively charged phospholipid, comprising a cyclic peptide sequence of the following formula (VIII):

Gly-RL1-Phe-RL2-P^1-Gly-Tyr-P^2-RL3-P^3-RL4-Q^1-RL5-Trp-RL6

(VIII)

wherein RL1 ~~and RL6~~ are independently selected from Lys, Orn and Arg; RL2 and RL3 are Arg; RL4, RL5, and RL6 ~~and RL5~~ are independently selected from Asp and Glu;

wherein P^1, P^2 and P^3 are independently selected from Ser and Thr; wherein Q^1 is selected from Gly and Met, said structures being bound.

22. (Previously Presented) A chemical assembly according to claim 21, wherein at least one of the chemical structures is a molecule of formula (VII).

23. (Previously Presented) A method for producing a chemical structure as defined in Claim 10, preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of

said cDNA.

24. (Previously Presented) The method according to claim 23, wherein the vector is a plasmid.

25. (Previously Presented) The method according to claim 23, wherein the vector is a pGEX-2T vector.

26. (Previously Presented) The method according to claim 23, wherein the appropriate host cell is *E. Coli.*

27. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 1.

28. (Previously Presented) A pharmaceutical composition comprising a chemical assembly as defined in Claim 21.

29. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 27.

30. (Previously Presented) A method for producing a material for covering thrombogenic biomaterial comprising incorporating a structure as claimed in Claim 1.

31. (Previously Presented) A labelling compound comprising a structure as defined in Claim 1 coupled with a labelling molecule.

32. (Previously Presented) A labelling compound comprising an assembly as defined in claim 21 coupled with a labelling molecule.

33. (Previously Presented) The compound according to claim 31, wherein the labelling molecule is selected from a fluorescent molecule, an avidin-biotin complex, a radioelement, and a paramagnetic compound.

34. (Previously Presented) A diagnostic kit comprising a compound according to Claim 31.

35. (Previously Presented) The ~~diagnose~~ diagnostic kit according to claim 34, further comprising an adequate reagent enabling said labeling molecule to be detected.

36. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising a structure according to Claim 1, coupled with a tracer.

37. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising an assembly according to Claim 21, coupled with a tracer.

38. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising a structure according to Claim 1, coupled with a tracer.

39. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising an assembly according to Claim 21, coupled with a tracer.

40. (Previously Presented) The chemical structure according to any of claim 2, wherein the platform is a portion of a domain of the annexin or of a modified domain of the annexin, comprising at least said residual ligands, RL1 to RL6, having said functions L1 to L6 for binding to the phospholipid respectively.

41. (Previously Presented) The chemical structure according to claim 40, wherein the annexin domain is selected from the domain 1 of annexin V corresponding to amino acid residues 16-91 of SEQ ID NO: 2, domain 2 of annexin I corresponding to amino acid residues 114-186 of SEQ ID NO: 1, domain 2 of annexin III corresponding to amino acid residues 90-162 of SEQ ID NO: 3, domain 1 of annexin IV corresponding to amino acid residues 15-85 of SEQ ID NO: 4, and domain 2 of annexin IV corresponding to amino acid residues 1-75 of SEQ ID NO: 5.

42. (Previously Presented) The chemical structure according to claim 41, wherein the residual ligands RL1 to RL6 respectively are either the residues Arg25, Lys29, Arg63, Asp68, Ser71 and Glu72 of domain 1 annexin V corresponding to amino acid residues 16-91 of SEQ

ID NO: 2 or residues Arg124, Lys128, Arg162, Asp167, Ser170 and Asp171 of domain 2 of annexin I corresponding to amino acid residues 114-186 of SEQ ID NO: 1, or residues Lys100, Lys104, Lys138, Asp143, Ser146 and Glu147 of domain 2 of annexin III corresponding to amino acid residues 90-162 of SEQ ID NO: 3, or residues Arg97, Lys101, Arg135, Asp140, Ser143 and Asp144 of domain 2 of annexin IV corresponding to amino acid residues 1-75 of SEQ ID NO: 5, or residues Arg24, Lys28, Arg62, Asp67, Ser70 and Glu71 of domain 1 of annexin IV corresponding to amino acid residues 15-85 of SEQ ID NO: 4.

43. (Previously Presented) The chemical structure according to claim 17, further comprising a calcium site where the calcium ion is complexed by this site forms one of the ligands of the negatively charged phospholipid.

44. (Previously Presented) The chemical structure according to Claim 2, said structures having an affinity for a phospholipid selected from a phosphatidylserine, a phosphatidylethanolamine, a phosphatidylinositol, a phosphatidic acid, and a cardiolipin.

45. (Previously Presented) The chemical structure according to Claim 13, said structures having an affinity for a phospholipid selected from a phosphatidylserine, a phosphatidylethanolamine, a phosphatidylinositol, a phosphatidic acid, and a cardiolipin.

46. (Previously Presented) The chemical structure according to Claim 17, said structures having an affinity for a phospholipid selected from a phosphatidylserine, a phosphatidylethanolamine, a phosphatidylinositol, a phosphatidic acid, and a cardiolipin.

47. (Previously Presented) The chemical structure according to Claim 18, said structures having an affinity for a phospholipid selected from a phosphatidylserine, a phosphatidylethanolamine, a phosphatidylinositol, a phosphatidic acid, and a cardiolipin.

48. (Previously Presented) A method for producing a chemical structure as defined in Claim 11, comprising preparing a cDNA comprising a coding sequence of bases for said

chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

49. (Previously Presented) A method for producing a chemical structure as defined in Claim 12, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

50. (Previously Presented) A method for producing a chemical structure as defined in Claim 13, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

51. (Previously Presented) A method for producing a chemical structure as defined in Claim 17, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

52. (Previously Presented) A method for producing a chemical structure as defined in Claim 18, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

53. (Previously Presented) A method for producing a chemical structure as defined in

Claim 48, comprising steps consisting of preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

54. (Previously Presented) A method for producing a chemical structure as defined in Claim 49, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

55. (Previously Presented) A method for producing a chemical structure as defined in Claim 50, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

56. (Previously Presented) A method for producing a chemical structure as defined in Claim 51, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

57. (Previously Presented) A method for producing a chemical structure as defined in Claim 52, comprising preparing a cDNA comprising a coding sequence of bases for said chemical structure, inserting the cDNA in an appropriate expression vector, transforming an appropriate host cell for replicating the plasmid and producing said structure by translation of said cDNA.

58. (Previously Presented) The method according to Claim 48, wherein the vector is a pGEX-2T vector.

59. (Previously Presented) The method according to Claim 49, wherein the vector is a pGEX-2T vector.

60. (Previously Presented) The method according to Claim 50, wherein the vector is a pGEX-2T vector.

61. (Previously Presented) The method according to Claim 51, wherein the vector is a pGEX-2T vector.

62. (Previously Presented) The method according to Claim 52, wherein the vector is a pGEX-2T vector.

63. (Previously Presented) The method according to claim 48, wherein the appropriate host cell is *E. Coli.*

64. (Previously Presented) The method according to claim 49, wherein the appropriate host cell is *E. Coli.*

65. (Previously Presented) The method according to claim 50, wherein the appropriate host cell is *E. Coli.*

66. (Previously Presented) The method according to claim 51, wherein the appropriate host cell is *E. Coli.*

67. (Previously Presented) The method according to claim 52, wherein the appropriate host cell is *E. Coli.*

68. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 2 and an inert material.

69. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 13 and an inert material.

70. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 17 and an inert material.

71. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 18 and an inert material.

72. (Previously Presented) A pharmaceutical composition comprising a chemical structure as defined in Claim 22 and an inert material.

73. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 68.

74. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 69.

75. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 70.

76. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 71.

77. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 28.

78. (Previously Presented) A method of treating a thrombosis, tumor or inflammation with the pharmaceutical composition claimed in Claim 72.

79. (Previously Presented) A method for producing a material for covering thrombogenic biomaterial comprising incorporating a structure as claimed in Claim 2.

80. (Previously Presented) A method for producing a material for covering thrombogenic biomaterial comprising incorporating a structure as claimed in Claim 13.

81. (Previously Presented) A method for producing a material for covering thrombogenic biomaterial comprising incorporating a structure as claimed in Claim 17.

82. (Previously Presented) A method for producing a material for covering thrombogenic biomaterial comprising incorporating a structure as claimed in Claim 18.

83. (Previously Presented) A labelling compound comprising a structure as defined in Claim 2 coupled with a labelling molecule.

84. (Previously Presented) A labelling compound comprising a structure as defined in Claim 13 coupled with a labelling molecule.

85. (Previously Presented) A labelling compound comprising a structure as defined in Claim 17 coupled with a labelling molecule.

86. (Previously Presented) A labelling compound comprising a structure as defined in Claim 18 coupled with a labelling molecule.

87. (Previously Presented) A labelling compound comprising an assembly as defined in claim 22 coupled with a labelling molecule.

88. (Previously Presented) The compound according to Claim 83, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

89. (Previously Presented) The compound according to Claim 84, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

90. (Previously Presented) The compound according to Claim 85, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

91. (Previously Presented) The compound according to Claim 86, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

92. (Previously Presented) The compound according to Claim 32, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

93. (Previously Presented) The compound according to Claim 87, wherein the labelling molecule is selected from a fluorescent molecule, the avidin-biotin complex, a radioelement, and a paramagnetic compound.

94. (Previously Presented) A diagnostic kit comprising a compound according to Claim 83.

95. (Previously Presented) A diagnostic kit comprising a compound according to Claim 84.

96. (Previously Presented) A diagnostic kit comprising a compound according to Claim 85.

97. (Previously Presented) A diagnostic kit comprising a compound according to Claim 86.

98. (Previously Presented) A diagnostic kit comprising a compound according to Claim 32.

99. (Previously Presented) A diagnostic kit comprising a compound according to Claim 87.

100. (Previously Presented) The diagnostic kit according to Claim 94, further comprising an adequate reagent enabling said labelling molecule to be detected.

101. (Previously Presented) The diagnostic kit according to Claim 95, further comprising an adequate reagent enabling said labelling molecule to be detected.

102. (Previously Presented) The diagnostic kit according to Claim 96, further comprising an adequate reagent enabling said labelling molecule to be detected.

103. (Previously Presented) The diagnostic kit according to Claim 97, further comprising an adequate reagent enabling said labelling molecule to be detected.

104. (Previously Presented) The diagnostic kit according to Claim 99, further comprising an adequate reagent enabling said labelling molecule to be detected.

105. (Previously Presented) The diagnostic kit according to Claim 99, further comprising an adequate reagent enabling said labelling molecule to be detected.

106. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising a structure according to Claim 2, coupled with a tracer.

107. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising a structure according to Claim 13, coupled with a tracer.

108. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising a structure according to Claim 17, coupled with a tracer.

109. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising a structure according to Claim 18, coupled with a tracer.

110. (Previously Presented) A kit for analyzing and detecting negative charges at the surface of cells, comprising an assembly according to Claim 22, coupled with a tracer.

111. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising a structure according to Claim 2, coupled with a tracer.

112. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising a structure according to Claim 13, coupled with a tracer.

113. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising a structure according to Claim 17, coupled with a tracer.

114. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising a structure according to Claim 18, coupled with a tracer.

115. (Previously Presented) A kit for analyzing and detecting microvesicles in blood at the surface of cells, comprising an assembly according to Claim 22, coupled with a tracer.

SUPPORT FOR THE AMENDMENTS

Claims 5, 13, 16, 18, and 21 have been amended.

The specification has been amended to correct the improper designation of "Ser171 of SEQ ID NO:1" with the proper "Asp171 of SEQ ID NO:1." The specification has also been amended to correct the definition of RL6.

The amendment of Claims 5, 13, 16, 18, and 21 and the specification to correct the definition of RL6 is supported by page 28, line 21 to page 30, line 2, Figures 6A-6D, and original Claims 4, 8, 12, and 42.

The amendment of Claim 16 and the specification to correct the improper designation of "Ser171 of SEQ ID NO:1" with the proper "Asp171 of SEQ ID NO:1" is supported by Figure 6A, the originally filed Sequence Listing, and page 12, line 13.

No new matter has been added by the present amendment.